

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/527,257C
Source: IFW16
Date Processed by STIC: 12/26/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 12/26/2006

PATENT APPLICATION: US/10/527,257C

TIME: 13:48:37

Input Set : A:\186353.txt

Output Set: N:\CRF4\12262006\J527257C.raw

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3 <110> APPLICANT: Shanghai Genomics, Inc.
5 <120> TITLE OF INVENTION: TUMOR TAG AND THE USE THEREOF
7 <130> FILE REFERENCE: 186353/US
9 <140> CURRENT APPLICATION NUMBER: 10/527,257C
10 <141> CURRENT FILING DATE: 2005-03-09
12 <150> PRIOR APPLICATION NUMBER: PCT/CN2002/000631
13 <151> PRIOR FILING DATE: 2002-09-09
15 <160> NUMBER OF SEQ ID NOS: 10
17 <170> SOFTWARE: PatentIn version 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 720
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(639)
29 <400> SEQUENCE: 1
30 atg gca gcg gcc gcc agc ccc gcg ttc ctt cta cgc ctc ccg ctt ctg      48
31 Met Ala Ala Ala Ala Ser Pro Ala Phe Leu Leu Arg Leu Pro Leu Leu
32 1          5          10          15
34 ctc ctg ctg tcc agc tgg tgc agg acc ggg ctg gcc gac cct cac tct      96
35 Leu Leu Leu Ser Ser Trp Cys Arg Thr Gly Leu Ala Asp Pro His Ser
36          20          25          30
38 ctt tgc tat gac atc acc gtc atc cct aag ttc aga cct gga cca cgg      144
39 Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro Gly Pro Arg
40          35          40          45
42 tgg tgt gcg gtt caa ggc cag gtg gat gaa aag act ttt ctt cac tat      192
43 Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr
44          50          55          60
46 gac tgt ggc agc aag aca gtc aca ccc gtc agt ccc ctg ggg aag aaa      240
47 Asp Cys Gly Ser Lys Thr Val Thr Pro Val Ser Pro Leu Gly Lys Lys
48 65          70          75          80
50 cta aat gtc aca acg gcc tgg aaa gca cag aac cca gta ctg aga gag      288
51 Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu
52          85          90          95
54 gtg gtg gac ata ctt aca gag caa ctg ctt gac att cag ctg gag aat      336
55 Val Val Asp Ile Leu Thr Glu Gln Leu Leu Asp Ile Gln Leu Glu Asn
56          100          105          110
58 tac ata ccc aag gaa ccc ctc acc ctg cag gcc agg atg tct tgt gag      384
59 Tyr Ile Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu
60          115          120          125
62 cag aaa gcc gaa gga cac ggc agt gga tct tgg cag ctc agt ttc gat      432
63 Gln Lys Ala Glu Gly His Gly Ser Gly Ser Trp Gln Leu Ser Phe Asp

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64      130      135      140
66 gga cag atc ttc ctc ctc ttt gac tca gaa aac aga atg tgg aca acg      480
67 Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu Asn Arg Met Trp Thr Thr
68 145      150      155      160
70 gtt cat cct gga gcc aga aag atg aaa gaa aag tgg gag aat gac aag      528
71 Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys
72      165      170      175
74 gat atg acc atg tcc ttc cat tac atc tca atg gga gac tgc aca gga      576
75 Asp Met Thr Met Ser Phe His Tyr Ile Ser Met Gly Asp Cys Thr Gly
76      180      185      190
78 tgg ctt gag gac ttc ttg atg ggc atg gac agc acc ctg gag cca agt      624
79 Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser
80      195      200      205
82 gca gga ggc aca gtc tgacccaaag ccatggccac caccctcagt ccctgcagcc      679
83 Ala Gly Gly Thr Val
84      210
86 tcctcctcat cctcccctgc ttcatacctcc ctggcatctg a      720
89 <210> SEQ ID NO: 2
90 <211> LENGTH: 213
91 <212> TYPE: PRT
92 <213> ORGANISM: Homo sapiens
94 <400> SEQUENCE: 2
96 Met Ala Ala Ala Ala Ser Pro Ala Phe Leu Leu Arg Leu Pro Leu Leu
97 1      5      10      15
100 Leu Leu Leu Ser Ser Trp Cys Arg Thr Gly Leu Ala Asp Pro His Ser
101      20      25      30
104 Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro Gly Pro Arg
105      35      40      45
108 Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr
109      50      55      60
112 Asp Cys Gly Ser Lys Thr Val Thr Pro Val Ser Pro Leu Gly Lys Lys
113 65      70      75      80
116 Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu
117      85      90      95
120 Val Val Asp Ile Leu Thr Glu Gln Leu Leu Asp Ile Gln Leu Glu Asn
121      100      105      110
124 Tyr Ile Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu
125      115      120      125
128 Gln Lys Ala Glu Gly His Gly Ser Gly Ser Trp Gln Leu Ser Phe Asp
129      130      135      140
132 Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu Asn Arg Met Trp Thr Thr
133 145      150      155      160
136 Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys
137      165      170      175
140 Asp Met Thr Met Ser Phe His Tyr Ile Ser Met Gly Asp Cys Thr Gly
141      180      185      190
144 Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser
145      195      200      205
148 Ala Gly Gly Thr Val

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149      210
152 <210> SEQ ID NO: 3
153 <211> LENGTH: 213
154 <212> TYPE: PRT
155 <213> ORGANISM: Homo sapiens
157 <400> SEQUENCE: 3
159 Met Ala Ala Ala Ala Ser Pro Ala Phe Leu Leu Arg Leu Pro Leu Leu
160 1          5          10          15
163 Leu Leu Leu Ser Ser Trp Cys Arg Thr Gly Leu Ala Asp Pro His Ser
164          20          25          30
167 Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro Gly Pro Arg
168          35          40          45
171 Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr
172          50          55          60
175 Asp Cys Gly Ser Lys Thr Val Thr Pro Val Ser Pro Leu Gly Lys Lys
176 65          70          75          80
179 Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu
180          85          90          95
183 Val Val Asp Ile Leu Thr Glu Gln Leu Leu Asp Ile Gln Leu Glu Asn
184          100         105         110
187 Tyr Ile Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu
188          115         120         125
191 Gln Lys Ala Glu Gly His Gly Ser Gly Ser Trp Gln Leu Ser Phe Asp
192          130         135         140
195 Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu Asn Arg Met Trp Thr Thr
196 145         150         155         160
199 Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys
200          165         170         175
203 Asp Met Thr Met Ser Phe His Tyr Ile Ser Met Gly Asp Cys Thr Gly
204          180         185         190
207 Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser
208          195         200         205
211 Ala Gly Gly Thr Val
212      210
215 <210> SEQ ID NO: 4
216 <211> LENGTH: 29
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial
220 <220> FEATURE:
221 <223> OTHER INFORMATION: ogligonucleotide
223 <400> SEQUENCE: 4
224 cggaattcat ggcagcggcc gccagcccc
227 <210> SEQ ID NO: 5
228 <211> LENGTH: 30
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial
232 <220> FEATURE:
233 <223> OTHER INFORMATION: oligonucleotide
235 <400> SEQUENCE: 5

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236 gccaaagcttg atgccagggga ggatgaagca 30
239 <210> SEQ ID NO: 6
240 <211> LENGTH: 34
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial
244 <220> FEATURE:
245 <223> OTHER INFORMATION: oligonucleotide
247 <400> SEQUENCE: 6
248 ccggaattcg accctcactc tctttgctat gaca 34
251 <210> SEQ ID NO: 7
252 <211> LENGTH: 30
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial
256 <220> FEATURE:
257 <223> OTHER INFORMATION: oligonucleotide
259 <400> SEQUENCE: 7
260 gccaaagcttg atgccagggga ggatgaagca 30
263 <210> SEQ ID NO: 8
264 <211> LENGTH: 21
265 <212> TYPE: DNA
266 <213> ORGANISM: Artificial
268 <220> FEATURE:
269 <223> OTHER INFORMATION: oligonucleotide
271 <400> SEQUENCE: 8
272 atggcagcgg ccgccagccc c 21
275 <210> SEQ ID NO: 9
276 <211> LENGTH: 24
277 <212> TYPE: DNA
278 <213> ORGANISM: Artificial
280 <220> FEATURE:
281 <223> OTHER INFORMATION: oligonucleotide
283 <400> SEQUENCE: 9
284 tcagatgcca gggaggatga agca 24
287 <210> SEQ ID NO: 10
288 <211> LENGTH: 60
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial
292 <220> FEATURE:
293 <223> OTHER INFORMATION: oligonucleotide
295 <400> SEQUENCE: 10
296 atggcagcgg ccgccagccc cgcgttcctt ctacgcctcc cgcttctgct cctgctgtcc 60

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RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5,6,7,8,9,10

VERIFICATION SUMMARY

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